In the specification:

Replace the original Sequence Listing with the substitute Sequence Listing filed herewith.

Paragraph beginning at page **3**, line **26**, has been amended as follows:

Fibrin formation from fibrinogen is a spontaneous self-assembly process resulting from the removal of fibrinopeptides by thrombin. Thrombin cleavage at the Arg16-Arg17 bond in the Aα chains and at the Arg14-Gly15 bond on the Bβ chains releases fibrinopeptides A and B, and exposes a polymerization site in the E domain consisting mainly of the N-terminus of the α chain. This N-terminus, which bears the sequence Gly-Pro-Arg-Val (SEQ ID NO:67), binds to a complementary polymerization site on two adjacent fibrinogen chains. End to end association of these fibrinogen molecules mediated by the D domains, creates a binding site for the E domain polymerization site, located on a third fibrinogen molecule. This DD(E) ternary complex forms a core that stabilizes the forming fibrin gel. The initial polymerization product is a linear, two-stranded protofibril. Lateral coalescence of these protofibrils results in thick fibers and a branched, three dimensional matrix. Lateral assembly is complex but probably involves the B polymerization site (the N-terminus of β) and trimolecular complexes formed through D domain interactions.

Paragraph beginning at page **18**, line **25**, has been amended as follows:

A particularly strong tetramer motif was observed having the sequence Tyr-Tyr-Gly (Thr/Ser/Val). The recurrent Tyr-Tyr-Gly-Thr (SEQ ID NO:4) motif observed in almost all of the specific isolated fibrin binding polypeptides led to selection of the particularly preferred embodiments herein: a fibrin binding loop comprising a polypeptide including the amino acid sequence: Cys-Xaa-Tyr-Tyr-Gly-Thr-Cys (SEQ ID NO:3), where Xaa is Asn, Asp, Gln, His, Ser or Trp; and a fibrin binding moiety comprising a polypeptide including the amino acid sequence Tyr-Tyr-Gly-Thr (SEQ ID NO:4).

Paragraph beginning at page **54**, line **10**, has been amended as follows:

A fibrin binding polypeptide was modified by replacement of Gly in the Tyr-Tyr-Gly-Thr (SEQ ID NO:4) motif with a D-amino acid (D-Ala). Gly is not asymmetric, and it can adopt conformations available to either an L- or a D-amino acid. If in the binding conformation of the peptide, Gly behaves like a D-amino acid, then its substitution by a D-amino acid should lock the peptide in this conformation and enhance the binding of the peptide.

Paragraph beginning at page **57**, line **11**, has been amended as follows:

Cyclization by forming an amide bond between the N-terminal amino group and the C-terminal carboxyl group represents an alternative for binding loop formation, e.g., instead of having disulfide formation between the cysteine positions. Also, some of the side chains lend themselves to cyclization via reaction of amino-functional side chains, such as with lysine or diaminopropanoic acid and the carboxylic acid side chain of aspartic acid. Such head-to-tail (I, II, SEQ ID NOs:68 and 69, respectively) and side-chain-to-side-chain (III, IV, SEQ ID NO:68) cyclic peptides bearing a central Tyr-Tyr-Gly-Thr (SEQ ID NO:4) moiety were prepared, having the structures shown in Table 12, below:

Paragraph beginning at page **59**, line **1**, has been amended as follows:

The dissociation constants (K_d) against the fibrin-derived peptide target, DD(E), were determined for the cyclic peptide of structure (II) (K_d>500) and a cyclic peptide according to structure (III) (K_d = 179). These results indicate that adjustment of the cyclic structure is necessary to correctly configure the Tyr-Tyr-Gly-Thr (SEQ ID NO:4) moiety for high affinity fibrin binding.